

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Marc G. ACHEN
Andrew F. WILKS
Steven A. STACKER
Kari ALITALO
- (ii) TITLE OF INVENTION: GROWTH FACTOR
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Evenson, McKeown, Edwards & Lenahan P.L.L.C.
(B) STREET: 1200 G Street, NW, Suite 700
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: United States of America
(F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: EVANS, Joseph D.
(B) REGISTRATION NO: 26,269
(C) REFERENCE/DOCKET NUMBER: 1064/42983
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (202) 628-8800
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(C) TELEX: N/A

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Human Breast
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGAATTCAGT GAAGTAAGAA AGACAAAGTG TTCATTGGAG ATTTTGTAGTA AGGGGCCAAC	60
AGAGCTGCTA AAGTCATGCT TCACTTAACG ATGGGGATAT GTTCGGAGAA ATGCATTGTT	120
AGGTGATTTT GTCGTTGTGC AAGCATCTTA GAGTACACTT AGACAAACCT AGCTGGTATA	180
ACCTAGGTGT GTAGTAGGAT ATATGGTATA GCCTATTGTT CCTAGGCTAC AAACCCATAC	240

AGCATGTTCC TGTACTGAAT ACTGAGGCAA CTGCAACACC GTGGTGAGTA TTTGTGTATC 300
 TAAACATACC TAAACATAGA AAAGATACAG TAAAAATATG GCATTATAGT CTTATGGGAC 360
 TACTGTCATA CATAAGTCC ATATATTGTT GACTGTGTAA TGTGGACCTG AATGTCATTA 420
 TGTGGCAGGC ACATGACTGT GTCGCTAACC TTTGCACAAG ATTACTGTAG GATTACATGA 480
 GATAGTTGTA AATAATTGGT GGGGTACTGG GCACCTAGTA GGTATGCATA CATGTTCCACC 540
 ATCATTATGG TTGTTTTAAA TCACCTAACC CAGGCCCTGC ACATAGTAAG ACATCAACAA 600
 ATTGTAGCTG CTACTATTTT GCGCATCTAA TCTTAATATC ATTTATTTTG TAGTCCTTGG 660
 ATGTTCCCTC CTTTATGACT TCTTTT TTTT TTGTTGCTCT TCCTTTAGCC CTCCATCCTC 720
 TACAGCTCAG CATCAGAAC A CTCTCTTTT AGACTCCGAT ATGGGGTCCT CCAAGAAAGT 780
 TACTCTCTCA GTGCTCAGCC GGGAGCAGTC GGAAGGGGTT GGAGCGAGGG TCCGGAGAAG 840
 CATTGGCAGA CCCGAGTTAA AAAATCTGGA TCCGTTTTTA CTGTTTGATG AATTTAAAGG 900
 AGGTAGACCA GGAGGATTTT CTGATCATCC ACATCGAGGT TTTGAAACAG TATCCTACCT 960
 CCTGGAAGGG GGCAGCATGG CCCATGAAGA CTTCTGTGGA CACACTGGTA AAATGAACCC 1020
 AGGAGATTTG CAGTGGATGA CTGCGGGCCG GGGCATTCTG CACGCTGAGA TGCCTTGCTC 1080
 AGAGGAGCCA GCCCATGGCC TACAACTGTG GGTTAATTTG AGGAGCTCAG AGAAGATGGT 1140
 GGAGCCTCAG TACCAGGAAC TGAAAAGTGA AGAAATCCCT AAACCCAGTA AGGATGGTGT 1200
 GACAGTTGCT GTCATTTCTG GAGAAGCCCT GGGAATAAAG TCCAAGGTTT ACACCTCGCAC 1260
 ACCAACCTTA TATTTGGA CTCAAATGGA CCCAGGAGCC AAACATTCCC AACCTATCCC 1320
 TAAAGGGTGG ACAAGCTTCA TTTACACGAT ATCTGGAGAT GTGTATATTG CCCTCTCTAT 1380
 ATCCCAGCAC AGGTATGCCC AGGGCAGGGT GCCTTTCAGC TTACAGAACA TTCAGTGAGG 1440
 GAAGAGAATA TGAACACCAG TCATGACACA TCCTGTGCAC AGATGAAAGT CCAGGCACCA 1500
 TTATGTGTTT TGATACCTCG CTAAGACGTT GGCAACCTCC ATACTGATAA AGGGATGGAG 1560
 CTACAGTGA CTCCAAGGGG AGCAGGAATC TGCCTATCTC CTGGGAGAAG GAAATGGAAG 1620
 GAGGGCCCGA TGATGCACAA CAAAAATAG AACCTCATCA CACAGCAGTG CTTGGAGAAG 1680
 GTGACAGTGT CCAAGTGGAG AACAAAGGATC CCAAGAGAAG CCACTTTGTC TTAATTGCTG 1740
 GGGAGCCATT AAGAGAACCA GTTATCCAAC ATGCGATCAT CTCAGTCCAC ATTGGAACGA 1800
 TCTGAACAGC AGATCAGGGC TGCTTCTAGT TTGGAGGAAC TACTTCGAAT TACTCACTCT 1860
 GAGGACTGGA AGCTGTGGAG ATGCAGGCTG AGGCTCAAAA GTTTTACCAG TATGGACTCT 1920
 CGCTCAGCAT CCCATCGGTC CACTAGGTTT GCGGCAACTT TCTATGACAT TGAAACACTA 1980
 AAAGTTATAG ATGAAGAATG GCAAAGAACT CAGTGCAGCC CTAGAGAAAC GTGCGTGGAG 2040
 GTGGCCAGTG AGCTGGGGAA GAGTACCAAC ACATTCTTCA AGCCCCCTTG TGTGAACGTG 2100
 TTCCGATGTG GTGGCTGTTG CAATGAAGAG AGCCTTATCT GTATGAACAC CAGCACCTCG 2160
 TACATTTCCA AACAGCTCTT TGAGATATCA GTGCCTTTGA CATCAGTACC TGAATTAGTG 2220
 CCTGTTAAAG TTGCCAATCA TACAGGTTGT AAGTGCTTGC CAACAGCCCC CCGCCATCCA 2280

TACTCAATTA TCAGAAGATC CATCCAGATC CCTGAAGAAG ATCGCTGTTC CCATTCCAAG 2340
AAACTCTGTC CTATTGACAT GCTATGGGAT AGCAACAAAT GTAAATGTGT TTTGCAGGAG 2400
GAAAATCCAC TCGCTGGAAC AGAAGACCAC TCTCATCTCC AGGAACCAGC TCTCTGTGGG 2460
CCACACATGA TGTTTGACGA AGATCGTTGC GAGTGTGTCT GTAAAACACC ATGTCCCAAA 2520
GATCTAATCC AGCACCCCAA AAAGTGCAGT TGCTTTGAGT GCAAAGAAAG TCTGGAGACC 2580
TGCTGCCAGA AGCACAAGCT ATTTACCCCA GACACCTGCA GCTGTGAGGA CAGATGCCCC 2640
TTTCATACCA GACCATGTGC AAGTGGCAAA ACAGCATGTG CAAAGCATTG CCGCTTTCCA 2700
AAGGAGAAAA GGGCTGCCCA GGGGCCCCAC AGCCGAAAGA ATCCTTGATT CAGCGTTCCA 2760
AGTTCCCCAT CCCTGTCATT TTTAACAGCA TGCTGCTTTG CCAAGTTGCT GTCAGTGT 2820
TTTTCCCAGG TGTAAAAAA AAAAAA 2846

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Xaa Cys Val Xaa Xaa Xaa Arg Cys Xaa Gly Cys Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE: Human Breast

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Arg Ser Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg
1 5 10 15

Ala Ala Ser Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp
20 25 30

Trp Lys Leu Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met
35 40 45

Asp Ser Arg Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe
50 55 60

Tyr Asp Ile Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr
 65 70 75 80
 Gln Cys Ser Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly
 85 90 95
 Lys Ser Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg
 100 105 110
 Cys Gly Gly Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser
 115 120 125
 Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr
 130 135 140
 Ser Val Pro Glu Leu Val Pro Val Lys Val Ala Asn His Thr Gly Cys
 145 150 155 160
 Lys Cys Leu Pro Thr Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg
 165 170 175
 Ser Ile Gln Ile Pro Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu
 180 185 190
 Cys Pro Ile Asp Met Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu
 195 200 205
 Gln Glu Glu Asn Pro Leu Ala Gly Thr Glu Asp His Ser His Leu Gln
 210 215 220
 Glu Pro Ala Leu Cys Gly Pro His Met Met Phe Asp Glu Asp Arg Cys
 225 230 235 240
 Glu Cys Val Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro
 245 250 255
 Lys Asn Cys Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys
 260 265 270
 Gln Lys His Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg
 275 280 285
 Cys Pro Phe His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala
 290 295 300
 Lys His Cys Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His
 305 310 315 320
 Ser Arg Lys Asn Pro
 325

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2029 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:
 - (F) TISSUE TYPE: Human Lung
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTGGGTTCC AGCTTTCTGT AGCTGTAAGC ATTGGTGGCC ACACCACCTC CTTACAAAGC 60
 AACTAGAACC TCGGCATAC ATTGGAGAGA TTTTFTAAT TTTCTGGACA TGAAGTAAAT 120
 TTAGAGTGCT TTCTAATTTT AGGTAGAAGA CATGTCCACC TTCTGATTAT TTTTGGAGAA 180
 CATTTTGATT TTTTTCATCT CTCTCTCCCC ACCCCTAAGA TTGTGCAAAA AAAGCGTACC 240
 TTGCCTAATT GAAATAATTT CATTGGATTT TGATCAGAAC TGATTATTTG GTTTTCTGTG 300
 TGAAGTTTTG AGGTTTCAAA CTTTCCTTCT GGAGAATGCC TTTTGAAACA ATTTTCTCTA 360
 GCTGCCTGAT GTCAACTGCT TAGTAATCAG TGGATATTGA AATATTCAAA ATGTACAGAG 420
 AGTGGGTAGT GGTGAATGTT TTCATGATGT TGTACGTCCA GCTGGTGCAG GGCTCCAGTA 480
 ATGAACATGG ACCAGTGAAG CGATCATCTC AGTCCACATT GGAACGATCT GAACAGCAGA 540
 TCAGGGCTGC TTCTAGTTTG GAGGAACTAC TTCGAATTAC TCACTCTGAG GACTGGAAGC 600
 TGTGGAGATG CAGGCTGAGG CTCAAAAGTT TTACCAGTAT GGACTCTCGC TCAGCATCCC 660
 ATCGGTCCAC TAGGTTTGCG GCAACTTTCT ATGACATTGA AACACTAAAA GTTATAGATG 720
 AAGAATGGCA AAGAACTCAG TGCAGCCCTA GAGAAACGTG CGTGGAGGTG GCCAGTGAGC 780
 TGGGGAAGAG TACCAACACA TTCTTCAAGC CCCCTTGTGT GAACGTGTTT CGATGTGGTG 840
 GCTGTTGCAA TGAAGAGAGC CTTATCTGTA TGAACACCAG CACCTCGTAC ATTTCCAAAC 900
 AGCTCTTTGA GATATCAGTG CCTTTGACAT CAGTACCTGA ATTAGTGCCT GTTAAAGTTG 960
 CCAATCATA AGGTTGTAAG TGCTTGCCAA CAGCCCCCG CCATCCATAC TCAATTATCA 1020
 GAAGATCCAT CCAGATCCCT GAAGAAGATC GCTGTTCCCA TTCCAAGAAA CTCTGTCTTA 1080
 TTGACATGCT ATGGGATAGC AACAAATGTA AATGTGTTTT GCAGGAGGAA AATCCACTTG 1140
 CTGGAACAGA AGACCACTCT CATCTCCAGG AACCAGCTCT CTGTGGGCCA CACATGATGT 1200
 TTGACGAAGA TCGTTGCGAG TGTGTCTGTA AAACACCATG TCCCAAAGAT CTAATCCAGC 1260
 ACCCCAAAA CTGCAGTTGC TTTGAGTGCA AAGAAAGTCT GGAGACCTGC TGCCAGAAGC 1320
 ACAAGCTATT TCACCCAGAC ACCTGCAGCT GTGAGGACAG ATGCCCCTTT CATAACAGAC 1380
 CATGTGCAAG TGGCAAAACA GCATGTGCAA AGCATTGCCG CTTTCCAAAG GAGAAAAGGG 1440
 CTGCCCAGGG GCCCCACAGC CGAAAGAATC CTTGATTAGC CGTTCCAAGT TCCCCATCCC 1500
 TGTCATTTTT AACAGCATGC TGCTTTGCCA AGTTGCTGTC ACTGTTTTTT TCCCAGGTGT 1560
 TAAAAAATA ATCCATTTTA CACAGACCA CAGTGAATCC AGACCAACCT TCCATTCA 1620
 CCAGCTAAGG AGTCCCTGGT TCATTGATGG ATGTCTTCTA GCTGCAGATG CCTCTGCGCA 1680
 CCAAGGAATG GAGAGGAGGG GACCCATGTA ATCCTTTTGT TTAGTTTTGT TTTGTTTTT 1740
 TGGTGAATGA GAAAGGTGTG CTGGTCATGG AATGGCAGGT GTCATATGAC TGATTACTCA 1800
 GAGCAGATGA GGAACACTGT AGTCTCTGAG TCCTTTGCTA ATCGCAACTC TTGTGAATTA 1860
 TTCTGATTCT TTTTATGCA GAATTTGATT CGTATGATCA GTACTGACTT TCTGATTACT 1920
 GTCCAGCTTA TAGTCTTCCA GTTTAATGAA CTACCATCTG ATGTTTCATA TTTAAGTGTA 1980
 TTTAAAGAAA ATAAACACCA TTATTCAAGC CAAAAAATA AAAAAAATA 2029

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(F) TISSUE TYPE: Human Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Tyr	Arg	Glu	Trp	Val	Val	Val	Asn	Val	Phe	Met	Met	Leu	Tyr	Val	
1				5				10						15		
Gln	Leu	Val	Gln	Gly	Ser	Ser	Asn	Glu	His	Gly	Pro	Val	Lys	Arg	Ser	
			20					25					30			
Ser	Gln	Ser	Thr	Leu	Glu	Arg	Ser	Glu	Gln	Gln	Ile	Arg	Ala	Ala	Ser	
		35					40					45				
Ser	Leu	Glu	Glu	Leu	Leu	Arg	Ile	Thr	His	Ser	Glu	Asp	Trp	Lys	Leu	
		50				55					60					
Trp	Arg	Cys	Arg	Leu	Arg	Leu	Lys	Ser	Phe	Thr	Ser	Met	Asp	Ser	Arg	
65					70					75					80	
Ser	Ala	Ser	His	Arg	Ser	Thr	Arg	Phe	Ala	Ala	Thr	Phe	Tyr	Asp	Ile	
			85					90						95		
Glu	Thr	Leu	Lys	Val	Ile	Asp	Glu	Glu	Trp	Gln	Arg	Thr	Gln	Cys	Ser	
			100					105						110		
Pro	Arg	Glu	Thr	Cys	Val	Glu	Val	Ala	Ser	Glu	Leu	Gly	Lys	Ser	Thr	
		115					120					125				
Asn	Thr	Phe	Phe	Lys	Pro	Pro	Cys	Val	Asn	Val	Phe	Arg	Cys	Gly	Gly	
		130				135					140					
Cys	Cys	Asn	Glu	Glu	Ser	Leu	Ile	Cys	Met	Asn	Thr	Ser	Thr	Ser	Tyr	
145					150					155					160	
Ile	Ser	Lys	Gln	Leu	Phe	Glu	Ile	Ser	Val	Pro	Leu	Thr	Ser	Val	Pro	
			165					170						175		
Glu	Leu	Val	Pro	Val	Lys	Val	Ala	Asn	His	Thr	Gly	Cys	Lys	Cys	Leu	
		180						185					190			
Pro	Thr	Ala	Pro	Arg	His	Pro	Tyr	Ser	Ile	Ile	Arg	Arg	Ser	Ile	Gln	
		195					200					205				
Ile	Pro	Glu	Glu	Asp	Arg	Cys	Ser	His	Ser	Lys	Lys	Leu	Cys	Pro	Ile	
		210				215					220					
Asp	Met	Leu	Trp	Asp	Ser	Asn	Lys	Cys	Lys	Cys	Val	Leu	Gln	Glu	Glu	
225					230					235				240		
Asn	Pro	Leu	Ala	Gly	Thr	Glu	Asp	His	Ser	His	Leu	Gln	Glu	Pro	Ala	
			245				250						255			
Leu	Cys	Gly	Pro	His	Met	Met	Phe	Asp	Glu	Asp	Arg	Cys	Glu	Cys	Val	
			260					265					270			

Cys Lys Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys
 275 280 285
 Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His
 290 300
 Lys Leu Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe
 305 310 315 320
 His Thr Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys
 325 330 335
 Arg Phe Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys
 340 345 350
 Asn Pro

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGAATGCC TTTTGCAACA CTTTTCAGTA GCTGCCTGGA AACAACTGCT TAGTCATCGG	60
TAGACATTTA AAATATTCAA AATGTATGGA GAATGGGGAA TGGGGGAATAT CCTCATGATG	120
TTCCATGTGT ACTTGGTGCA GGGCTTCAGG AGCGAACATG GACCAGTGAA GGATTTTTTCT	180
TTTGAGCGAT CATCCCGGTC CATGTTGGAA CGATCTGAAC AACAGATCCG AGCAGCTTCT	240
AGTTTGGAGG AGTTGCTGCA AATCGCGCAC TCTGAGGACT GGAAGCTGTG GCGATGCCGG	300
TTGAAGCTCA AAAGTCTTGC CAGTATGGAC TCACGCTCAG CATCCCATCG CTCCACCAGA	360
TTTGCGGCAA CTTTCTATGA CACTGAAACA CTAAAAGTTA TAGATGAAGA ATGGCAGAGG	420
ACCCAATGCA GCCCTAGAGA GACATGCGTA GAAGTCGCCA GTGAGCTGGG GAAGACAACC	480
AACACATTCT TCAAGCCCCC CTGTGTAAAT GTCTTCCGGT GTGGAGGCTG CTGCAACGAA	540
GAGGGTGTGA TGTGTATGAA CACAAGCACC TCCTACATCT CCAAACAGCT CTTTGAGATA	600
TCAGTGCCTC TGACATCAGT GCCCGAGTTA GTGCCTGTTA AAATTGCCAA CCATACGGGT	660
TGTAAGTGCT TGCCCACGGG CCCCCGCCAT CCTTACTCAA TTATCAGAAG ATCCATT CAG	720
ACCCCAGAAG AAGATGAATG TCCTCATTCC AAGAACTCT GTCTTATTGA CATGCTGTGG	780
GATAACACCA AATGTAAATG TGTTTTGCAA GACGAGACTC CACTGCCTGG GACAGAAGAC	840
CACTCTTACC TCCAGGAACC CACTCTCTGT GGACCGCACA TGACGTTTGA TGAAGATCGC	900
TGTGAGTGCG TCTGTAAAGC ACCATGTCCG GGAGATCTCA TTCAGCACCC GGAAAAC TGC	960

AGTTGCTTTG AGTGCAAAGA AAGTCTGGAG AGCTGCTGCC AAAAGCACAA GATTTTTCAC 1020
 CCAGACACCT GCAGCTGTGA GGACAGATGT CCTTTTCACA CCAGAACATG TGCAAGTAGA 1080
 AAGCCAGCCT GTGGAAGCA CTGGCGCTTT CCAAAGGAGA CAAGGGCCCA GGGACTCTAC 1140
 AGCCAGGAGA ACCCTTGATT CAACTTCCTT TCAAGTCCCC CCATCTCTGT CATTTTAAAC 1200
 AGCTCACTGC TTTGTCAAGT TGCTGTCACT GTTGCCCACT ACCCCTTGAA CATGTGCAAA 1260
 CACAGACACA CACACACACA CACACACAGA GCAACTAGAA TTATGTTTTT TAGGTGCTGC 1320
 CTAAG 1325

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
 (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAACTTTGCT TCTGGAGAAT GCCTTTTGCA ACACTTTTCA GTAGCTGCCT GGAAACAAC 60
 GCTTAGTCAT CGGTAGACAT TTAAATATT CAAATGTAT GGAGAATGGG GAATGGGGAA 120
 TATCCTCATG ATGTTCCATG TGTACTTGGT GCAGGGCTTC AGGAGCGAAC ATGGACCAGT 180
 GAAGCGATCA TCCCGGTCCA TGTGGAACG ATCTGAACAA CAGATCCGAG CAGCTTCTAG 240
 TTTGGAGGAG TTGCTGCAAA TCGCGCACTC TGAGGACTGG AAGCTGTGGC GATGCCGGTT 300
 GAAGCTCAAA AGTCTTGCCA GTATGGACTC ACGCTCAGCA TCCCATCGCT CCACCAGATT 360
 TCGGGCAACT TTCTATGACA CTGAAACACT AAAAGTTATA GATGAAGAAT GGCAGAGGAC 420
 CCAATGCAGC CCTAGAGAGA CATGCGTAGA AGTCGCCAGT GAGCTGGGGA AGACAACCAA 480
 CACATTCTTC AAGCCCCCTT GTGTAAATGT CTTCCGGTGT GGAGGCTGCT GCAACGAAGA 540
 GGGTGTGATG TGTATGAACA CAAGCACCTC CTACATCTCC AAACAGCTCT TTGAGATATC 600
 AGTGCCTCTG ACATCAGTGC CCGAGTTAGT GCCTGTTAAA ATTGCCAACC ATACGGGTTG 660
 TAAGTGCTTG CCCACGGGCC CCCGCCATCC TTA CTCAATT ATCAGAAGAT CCATT CAGAC 720
 CCCAGAAGAA GATGAATGTC CTCATTCCAA GAAACTCTGT CCTATTGACA TGCTGTGGGA 780
 TAACACCAAA TGTAATGTG TTTTGCAAGA CGAGACTCCA CTGCCTGGGA CAGAAGACCA 840
 CTCTTACCTC CAGGAACCCA CTCTCTGTGG ACCGCACATG ACGTTTGATG AAGATCGCTG 900
 TGAGTGCGTC TGTAAGCAC CATGTCCGGG AGATCTCATT CAGCACCCGG AAAACTGCAG 960
 TTGCTTTGAG TGCAAAGAAA GTCTGGAGAG CTGCTGCCAA AAGCACAAGA TTTTTCACCC 1020
 AGACACCTGC AGGTCAATGG TCTTTTCGCT TTCCCTTAA CTTGGTTTAC TGATGACATT 1080

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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Met Tyr Gly Glu Trp Gly Met Gly Asn Ile Leu Met Met Phe His Val
1           5           10           15
Tyr Leu Val Gln Gly Phe Arg Ser Glu His Gly Pro Val Lys Asp Phe
20           25           30
Ser Phe Glu Arg Ser Ser Arg Ser Met Leu Glu Arg Ser Glu Gln Gln
35           40           45
Ile Arg Ala Ala Ser Ser Leu Glu Glu Leu Leu Gln Ile Ala His Ser
50           55           60
Glu Asp Trp Lys Leu Trp Arg Cys Arg Leu Lys Leu Lys Ser Leu Ala
65           70           75           80
Ser Met Asp Ser Arg Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala
85           90           95
Thr Phe Tyr Asp Thr Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln
100          105          110
Arg Thr Gln Cys Ser Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu
115          120          125
Leu Gly Lys Thr Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val
130          135          140
Phe Arg Cys Gly Gly Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn
145          150          155          160
Thr Ser Thr Ser Tyr Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro
165          170          175
Leu Thr Ser Val Pro Glu Leu Val Pro Val Lys Ile Ala Asn His Thr
180          185          190
Gly Cys Lys Cys Leu Pro Thr Gly Pro Arg His Pro Tyr Ser Ile Ile
195          200          205
Arg Arg Ser Ile Gln Thr Pro Glu Glu Asp Glu Cys Pro His Ser Lys
210          215          220
Lys Leu Cys Pro Ile Asp Met Leu Trp Asp Asn Thr Lys Cys Lys Cys
225          230          235          240
Val Leu Gln Asp Glu Thr Pro Leu Pro Gly Thr Glu Asp His Ser Tyr
245          250          255
Leu Gln Glu Pro Thr Leu Cys Gly Pro His Met Thr Phe Asp Glu Asp
260          265          270

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Arg Cys Glu Cys Val Cys Lys Ala Pro Cys Pro Gly Asp Leu Ile Gln
 275 280 285
 His Pro Glu Asn Cys Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Ser
 290 295 300
 Cys Cys Gln Lys His Lys Ile Phe His Pro Asp Thr Cys Ser Cys Glu
 305 310 315 320
 Asp Arg Cys Pro Phe His Thr Arg Thr Cys Ala Ser Arg Lys Pro Ala
 325 330 335
 Cys Gly Lys His Trp Arg Phe Pro Lys Glu Thr Arg Ala Gln Gly Leu
 340 345 350
 Tyr Ser Gln Glu Asn Pro
 355

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (F) TISSUE TYPE: Mouse Lung

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Tyr Gly Glu Trp Gly Met Gly Asn Ile Leu Met Met Phe His Val
 1 5 10 15
 Tyr Leu Val Gln Gly Phe Arg Ser Glu His Gly Pro Val Lys Arg Ser
 20 25 30
 Ser Arg Ser Met Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
 35 40 45
 Ser Leu Glu Glu Leu Leu Gln Ile Ala His Ser Glu Asp Trp Lys Leu
 50 55 60
 Trp Arg Cys Arg Leu Lys Leu Lys Ser Leu Ala Ser Met Asp Ser Arg
 65 70 75 80
 Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Thr
 85 90 95
 Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
 100 105 110
 Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Thr Thr
 115 120 125
 Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
 130 135 140
 Cys Cys Asn Glu Glu Gly Val Met Cys Met Asn Thr Ser Thr Ser Tyr
 145 150 155 160
 Ile Ser Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro
 165 170 175

Glu Leu Val Pro Val Lys Ile Ala Asn His Thr Gly Cys Lys Cys Leu
 180 185 190
 Pro Thr Gly Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln
 195 200 205
 Thr Pro Glu Glu Asp Glu Cys Pro His Ser Lys Lys Leu Cys Pro Ile
 210 215 220
 Asp Met Leu Trp Asp Asn Thr Lys Cys Lys Cys Val Leu Gln Asp Glu
 225 230 235 240
 Thr Pro Leu Pro Gly Thr Glu Asp His Ser Tyr Leu Gln Glu Pro Thr
 245 250 255
 Leu Cys Gly Pro His Met Thr Phe Asp Glu Asp Arg Cys Glu Cys Val
 260 265 270
 Cys Lys Ala Pro Cys Pro Gly Asp Leu Ile Gln His Pro Glu Asn Cys
 275 280 285
 Ser Cys Phe Glu Cys Lys Glu Ser Leu Glu Ser Cys Cys Gln Lys His
 290 295 300
 Lys Ile Phe His Pro Asp Thr Cys Arg Ser Met Val Phe Ser Leu Ser
 305 310 315 320
 Pro

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GGGCTGCTTC TAGTTTGGAG 20

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(vi) ORIGINAL SOURCE:
(F) TISSUE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CACTCGCAAC GATCTTCGTC 20